



Docket No.: CL000651

Serial No.: 09/727,770

Inventors: LI, Zhenya et al.

Title: ISOLATED HUMAN TRANSPORTER...

```
1 TCACAGAACA TGTCCAACAA CAGCCCCGAG TATGCTTTGG TTTTCACCAT
51 CTCGGGTGCT ATGGCCACCA TGGTCTCCAG TGGCCTGGGT GCTGCCTGTG
101 GCATGGCCAA GAATGGCACC GGCATCATGG CCATGTCTGT CATGTGGCCA
151 GAGCTGATCC ACATGAAATC CATCATCCCA GTGGTCATGG CTGGTATCAT
201 CACCATCTAT GGCCTAGTGG CGGCTGTCCC CCCTGCCAAC TCCCTGAATG
251 ATGACAACAG TCTCTATAGC AGTTTCCTCC AGCTGGGCGC TGGCCTGAGT
301 GGCCTGGCAG CCGGCTTTGC CATCGTCATC GTGGGGGACA CTGGCAAGTG
351 TGGCACTGCC CAGCAGCCCC GACTATTTGT AGGCATGATA CTGATCCTCA
401 TCTTTGCCAA GGTGCTCATT CTCTCCACAA AGCAGCCCCT CTCAAAACCC
451 ACCAGTCACA GAATACGATG TAAAGACCAC CCCTCCTCAT TCCGGAACAA
501 ACAGCCTGAC ACGCATGTGC TGGGCAGCTG GCCCTCAGTA GTTGATCTTC
551 TAAGTGATCA GTGTCCTCGT GTTCATCGTC TGTGGCCAG GCCTTGCCCC
601 CTCCCGCCCC ATGCTGTGGA CATCTGAACC TAC
```

(SEQ ID NO:1)

FEATURES:

5'UTR: 1-9

Start Codon: 10

Stop Codon: 625

3'UTR: 628

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FIGURE 1A



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HOMOLOGOUS PROTEINS:
Top BLAST Hits:

	Score	E
gi 4502313 ref NP_001685.1 ATPase, H ⁺ transporting, lysosomal ...	181	5e-45
gi 137477 sp P23956 VATL_BOVIN VACUOLAR ATP SYNTHASE 16 KD PROT...	180	8e-45
gi 227919 prf 1713409A H ATPase 16K [Bos taurus]	180	1e-44
gi 3024812 sp O18882 VATL_SHEEP VACUOLAR ATP SYNTHASE 16 KD PRO...	178	3e-44
gi 418179 sp Q03105 VATL_TORMA VACUOLAR ATP SYNTHASE 16 KD PROT...	175	5e-43
gi 6753144 ref NP_033859.1 ATPase-like vacuolar proton channel...	174	8e-43
gi 67954 pir PXBOV6 H ⁺ -transporting ATPase (EC 3.6.1.35), vacu...	165	3e-40
gi 137478 sp P23380 VATL_DROME VACUOLAR ATP SYNTHASE 16 KDA PRO...	157	1e-37
gi 3334403 sp O16110 VATL_AEDAE VACUOLAR ATP SYNTHASE 16 KD PRO...	156	2e-37
gi 1718095 sp P55277 VATL_HELVI VACUOLAR ATP SYNTHASE 16 KD PRO...	153	1e-36
gi 401334 sp P31403 VATL_MANSE VACUOLAR ATP SYNTHASE 16 KD PROT...	153	1e-36
gi 10442628 gb AAG17394.1 AF277150_1 (AF277150) V-ATPase 16 kD ...	151	5e-36
gi 7294725 gb AAF50062.1 (AE003544) CG7547 gene product [Droso...	151	7e-36
gi 2493142 sp Q26250 VATL_NEPNO VACUOLAR ATP SYNTHASE 16 KD PRO...	150	2e-35
gi 251354 gb AAB22509.1 vacuolar H(+)-ATPase proteolipid subun...	150	2e-35
gi 2493143 sp Q00607 VATL_CANTR VACUOLAR ATP SYNTHASE 16 KD PRO...	144	9e-34

BLAST to dbEST:

	Score	E
gi 9336427 /dataset=dbest /taxon=960...	165	1e-38
gi 6359805 /dataset=dbest /taxon=9606 ...	165	1e-38
gi 9134224 /dataset=dbest /taxon=9606...	165	1e-38
gi 10219114 /dataset=dbest /taxon=96...	165	1e-38
gi 9347217 /dataset=dbest /taxon=960...	165	1e-38
gi 9152104 /dataset=dbest /taxon=9606...	161	2e-37
gi 9894156 /dataset=dbest /taxon=960...	155	1e-35

EXPRESSION INFORMATION FOR MODULATORY USE:

library source:

Expression information from BLAST dbEST hits:

gi|9336427 Human uterus
gi|6359805 Human fetal liver
gi|9134224 Human brain
gi|10219114 Human lung
gi|9347217 Human placenta
gi|9152104 Human skin
gi|9894156 Human ovary

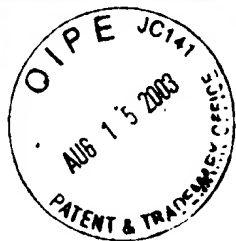
Expression information from PCR-based tissue screening panels

Human Bone marrow
Human Brain
Human Colon
Human Fetal Brain
Human fetal heart
Human Fetal kidney
Human fetal liver
Human Heart
Human Kidney
Human Liver
Human Lung
Human Pancreas
Human Placenta
Human Prostate
Human Skeletal Muscle
Human Small Intestine
Human Spleen
Human Testis

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1 MSNNSPEYAL VFTISGAMAT MVSSGLGAAC GMAKNGTGIM AMSVMWPELI
51 HMKSIIPVVM AGIITIYGLV AAVPPANSLN DDNSLYSSFL QLGAGLSGLA
101 AGFAIVIVGD TGKCGTAQQP RLFVGMILIL IFAKVLILST KQPLSKPTSH
151 RIRCKDHPSS FRNKQPDTHV LGSWPSVVDL LSVQCPRVHR LLARPCPLPP
201 HAVDI
(SEQ ID NO:2)

FEATURES:

Functional domains and key regions:

[1] PDOC00001 PS00001 ASN_GLYCOSYLATIONN-glycosylation site
35-38 NGTG

[2] PDOC00005 PS00005 PKC_PHOSPHO_SITEProtein kinase C phosphorylation site

Number of matches: 4

1	111-113	TGK
2	139-141	STK
3	149-151	SHR
4	160-162	SFR

[3] PDOC00006 PS00006 CK2_PHOSPHO_SITECasein kinase II phosphorylation site

Number of matches: 2

1	78-81	SLND
2	176-179	SVVD

[4] PDOC00008 PS00008 MYRISTYLN-myristoylation site

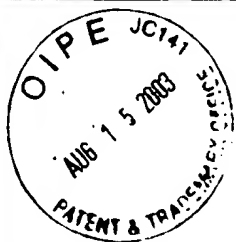
Number of matches: 8

1	16-21	GAMATM
2	25-30	GLGAAC
3	27-32	GAACGM
4	31-36	GMAKNG
5	68-73	GLVAAV
6	93-98	GAGLSG
7	98-103	GLAAGF
8	172-177	GSWPSV

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Membrane spanning structure and domains:

Helix	Begin	End	Score	Certainty
1	14	34	1.889	Certain
2	37	57	0.733	Putative
3	60	80	2.030	Certain
4	95	115	1.775	Certain
5	127	147	1.699	Certain

BLAST Alignment to Top Hit:

>gi|4502313|ref|NP_001685.1| ATPase, H+ transporting, lysosomal
 (vacuolar proton pump) 16kD
 >gi|137479|sp|P27449|VATL_HUMAN VACUOLAR ATP SYNTHASE 16
 KD PROTEOLIPID SUBUNIT >gi|107394|pir||A39367
 H+-transporting ATPase (EC 3.6.1.35) chain PKD1 - human
 >gi|189676|gb|AAA60039.1| (M62762) vacuolar H+ ATPase
 proton channel subunit [Homo sapiens]
 Length = 155

Score = 181 bits (455), Expect = 5e-45
 Identities = 110/153 (71%), Positives = 114/153 (73%), Gaps = 14/153 (9%)

Query: 2 SNNSPEYALVFTISGAMATMVSSGLGAACGMAKNGTGIMAMSVMWPELIHMKSIIPVVMA 61
 S + PEYA F + GA A MV S LGAA G AK+GTGI AMSVM PE I MKSIIPVVMA
 Sbjct: 4 SKSGPEYASFFAVMGASAAAMVFSALGAAYGTAKSGTGIAAMSVMRPEQI-MKSIIPVVMA 62

Query: 62 GIITIYGLVAAPPPANSLNDDNSLYSSFLQLGA----GLSGLAAGFAIVIVGDTGKCGTA 117
 GII IYGLV AV ANSLNDD SLY SFLQLGA GLSGLAAGFAI IVGD G GTA
 Sbjct: 63 GIIAIYGLVVAVLIANSNDDISLYKSFLQLGAGLSVGLSGLAAGFAIGIVGDAGVRGTA 122

Query: 118 QQPRLFVGMILILIFAKV-----LILSTK 141
 QQPRLFVGMILILIFA+V LILSTK

Sbjct: 123 QQPRLFVGMILILIFAEVGLGLYGLIVALILSTK 155 (SEQ ID NO:4)

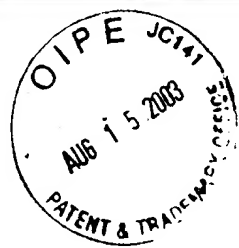
Hmmer search results (Pfam):

Model	Description	Score	E-value	N
PF00137	ATP synthase subunit c	14.8	0.028	2

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
PF00137	1/2	12	73	1	65	7.6	2.4
PF00137	2/2	89	133	1	53	14.6	0.031

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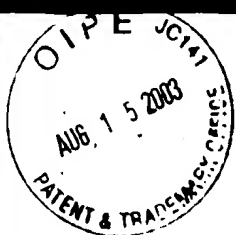


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1 GCTGTGGGGC CAGGAAAAGG AGAGAAGGTG AAACCCCGT CAGTCCCTCA
51 CAATCAGCAC GTGGAAATCT AGAAATGCAG GAGAGGCTG GACTCATGGT
101 GGAATCCAGA ATGAAAGAGG TGGACGACTG AATGAGCAGA AGGAGGCAAG
151 CACCAGAGGC TTGGGGGTCA CATTTCCTGG AAGTGGCTG GAGCTGGCAG
201 ATGAGAACTC TGGCTACCCG TCCTCATTC ACTAACAGTA GCTCCTCTAA
251 CGACATGCCC CTTCCTCTG TACCCGCTC CGCATGCGGC AAGTAGTTCC
301 CGGACGCGAC CCTTCCCCCT GTACCCCGCT CCGCATGGGG CCAGTAGTTC
351 CCGGACGCGC CCCTTCCCTC TGTACCCGCT TCCGCATGCG GCAAGTAGTT
401 CCCGGACGCG CCCCTTCCCT CTGTACCCGG CTCCGCATGC GGAAAGTAGT
451 TCCTACGGTG TTGGTTTTGC ATGTAGATGA AACCCCTTGA GGGGTAAAGG
501 TTTTTTTTTT AAGTACTTTA GCAAATGCAA ACTGTTATTA TCAATATTAG
551 CCAGCATCTT TTTTTTTTTT TTTTTTTTTT TTTTGTAGAT GGAGTTTCGC
601 TCTTGTCCAC CAGGCTGGAG TGCAATGGCA AAATCTAGGC TCACTGCAAC
651 CTCCGCTCC CAAGTCAAG CGATTCTCCT GCCTCAGCCT CCCAGGTAGC
701 TGGGATTACA GGCCTGTGCA ACCACACCCA GCTAATTTTT GTATTTTTAG
751 TAGAGACAGG GTTTCACCAT GTTGGCCAGG CTGGTCTCGA ACTCCTGACC
801 TCATGTGATC CATCCGCTC AGCCTCCCAA AGTGCTGGGA TTACGTAGCC
851 AGTGCTTTT GTCAAATAAT GCTCCTGGTT TATAAGTGCC
901 CCTGGCTCTA CCTTCTGGGT GCTCAGACAC CAACACAGAG AGAACAGAAT
951 TAACATCCTG AGAAGTTACA TATGCTAAAA TATAAAGAGT AAGATTGTGA
1001 GGAAACTGCA GGGGAAGCAG GTAGGTTAGG AAAAGGTATC CTCACCTTTC
1051 TGCTGACCGA TGAGTCATAA TTCTTGAATT TCGGTGCTGG AAAGGTCCAT
1101 TAAGCATTCC AGGAGATTCT AGGGAGCTTC CAGAATGGTA GAAGAACTGG
1151 AACCATAAAG CCTGGGGAAG GGATGGAAGT CCTTGGGAAA GAAGCACTAA
1201 ACAGCCAGT GGAGACAAGG AAGGACTGGT CTCTCCTGTG CTTCGAGCCC
1251 AGCAATGATT ATTCCTCAG ATATGCCCG GCAGGTCCTG CTGCTAGAGC
1301 CAGTGCTGTT CCCAGACCCA GGCAAGGTGC CATCCTACCC CTGACAGGAA
1351 ACAGGGCAGG AGGTGGGGCT GCCCCGGGTG CCTGGTGTG GGAGGGGCCG
1401 GGGGGAATCC CGGGTGTGAG GAGGACAAGG CAGAGTCAGC TAGCTGTGAG
1451 GCTAGGGGAG AAGACCTCTC TAGTCTGGGA GAGACCCCTC CTTTCTAGC
1501 TCCTTGTA CTCAAAAAGG CAGGCTTCCT GCTGTTACTA ACCATACCAG
1551 GACTGACTAT ACAGCAGCCA GAAAGATTCT GAGAAACCTG TGATAGAGAA
1601 AAACAGATGC GGAAGCGGGA GAAGAGAAAT TCATAGGACA CTAGGGAAAG
1651 AGAATGGGAA CTTGTGGTCT AAAGAGGGAA CCAAGTCTGG CCAACATGGT
1701 GAAACCCCAT TCTATTACA AATACAAAAA TTAGCTGGGC ATGGTAGTGC
1751 ATGCCTGTAA TCCCAGCTAC TCAGGAGGGT AAGGCATGAG AATCACTTGA
1801 GACTGGGAGG CGGAGGTGTC AGTGAGCCGA GACTGCACCA CTGCACTCCA
1851 GCCTGGGCAA CAGAGCAAGA CCTCGTCTCA AAAAAAAAAA AAAATTAAAT
1901 TTAATAATAA AAAAAATAAA CAGGGAACCA ACAAGAGCTG GCAGAACAGA
1951 ATAAAGTCTC AAGCCAAATA ACTCCCTTGC CTTGGAAGAA CAAGGCTGCC
2001 AGCGTCTTGG AGCCTCTGTT TATCGGGTAC CAGTTCAAAG GACAGTGAGC
2051 CTGAGCTGGC CTGGGAGGCC CTCCCCCTC CCAGATGAAA ACAATAGGCC
2101 TGTTTCTCTG GTACTTTCCT GTAATCCAGA AGGCCACAC AGAGAGGAAG
2151 AGGGGGGCAA AGGCAGTGGC TATACCCAGT GGGGGAGGGG ATATTTAGCC
2201 TCCCATAAAT TCATCAGCTC CCTTAAAGAC ACCCCAAAAC ACCAACATC
2251 TAAGTGTTAA AATAGTGACT GCTATGCAAA TGGAGCTTTA AAACCTATCC
2301 CTTAGGCCAC GTACCACAG ATTACTAACC CTAAACCCA TCTGTAGGAG
2351 ATATTCTGAA GCCACCACAG GGGAAGGGAT AAGGGCTGA GAGACAAAGG
2401 ACAGATGGGG TCTCCCCAAC AATTTAAGTT AAGTTCACA AGGATACAGT
2451 ACTGGCAGAG ATTTGGAAGT AGGGGCAAGT ATTCTGACAG AAGGGTGGTG
2501 TCTTAGGCAC CCTTCAATTA GGAGTAGCTA AAGGCTGTGT GTGTGTGTG
2551 GTGTGTGCAT AAGAAAAGAA ATAGGAGGGT GTGTGTGTGG TAAGAAAGAG
2601 CATCTTGGCT GGGCGCGGTG GCTCACCCCT ATAATCGCAG CACTTTGGGA
2651 TGCCAAGGCT GGCAGATTGC CTGAGCTCAG GAGTTTGAGA CCATACGGGG
2701 CAACATGGTG AAACCCATC TCTACTAAAA ATACAAAAAA TTAGCTGGGC
2751 ATGGTGGTGC GTGCCTATAG TTCCAGCTAC TCGGGAGGCT GAGGCATGAG
2801 AATGGCTTGA GCCCTGGAGG CAGAGGTTGA AGTGAGCTGA GATCGCACCA
2851 TTGCATTCCA GCTTGGGCTA CAGAGTGACA CTCCATCTCA AAAAAAAAAA
2901 AAAAAAAAAA ATCTTTGCTG ATCTTTGCTG CCACTAGTCC ACTGCTTTG
2951 CACTCACTCT CTGCCATGCC CATCCTTGTG CCCCTCCCA CTCACAGACA
3001 TGTCCAACAA CAGCCCCGAG TATGCTTTGG TTTTCACCAT CTCGGGTGCT
3051 ATGGCCACCA TGGTCTCCAG TGGCCTGGGT GCTGCCTGTG GCATGGCCAA
3101 GAATGGCACC GGCATCATGG CCATGTCTGT CATGTGGCCA GAGCTGATCC
3151 ACATGAAGTC CATCATCCCA GTGGTCATGG CTGGTATCAT CACCATCTAT
3201 GGCCTAGTGG CGGCTGTCCC CCCTGCCAAC TCCCTGAATG ATGACAACAG
3251 TCTCTATAGC AGTTTCTCTC AGCTGGGCGC TGGCCTGAGT GGCCTGGCAG
3301 CCGGCTTTGC CATCGTCATC GTGGGGGACA CTGGCAAGTG TGGCACTGCC
3351 CAGCAGCCCC GACTATTGTG AGGCATGATA CTGATCCTCA TCTTTGCCAA
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FIGURE 3A

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3401 GGTGCTCATT CTCTCCACAA AGCAGCCCCT CTCAAAACCC ACCAGTCACA
3451 GAATACGATG TAAAGACCAC CCCTCCTCAT TCCGGAACAA ACAGCCTGAC
3501 ACGCATGTGC TGGGCAGCTG GCCCTCAGTA GTTGATCTTC TAAGTGATACA
3551 GTGTCCTCGT GTTCATCGTC TGTTGGCCAG GCCTTGCCCC CTCCCCCCCC
3601 ATGCTGTGGA CATCTGAACC TACTCATCAC CCATCCAGGT CCCCAGACCAG
3651 TGAGGACTCA GGCCCTGGA TGCCCCACCC ATCTCCCTTG AGTACTCTAT
3701 GTATAAGGAT GAATTAGAGT TGTCATTTTC TCTTCATTAG ATATTTATAA
3751 AGATTTGGCC TGTCCATACC CCTGTGGAGC AGCCCTCATC TCCCACCTAT
3801 CTGTCACTGC ATGGAGGTTT CCATTGCGGA GGCTCCTTGG ATGGAACCAC
3851 CCTCTCCAGC CCGCGCTGCC AGGCCCTGTG CGGCAGCTGT GTCTGATAAA
3901 GTTCTCAGAT GTCGGGGGAG GGAAAGAAAA AAAAAAGAGA GTGTGAGTAC
3951 GTAAGAGAGA GAAAACGGGA GTGGGTGTGT GAGCTGGAGA CAGGGAAGTG
4001 GCAGGAAAAG TCTGATAAGA TCACCTCCTT CCTACCCAAG CAGAGATACT
4051 GGACAGCTCC CCTCAAGGAC CCAGAGGGTA AGTAGAGCGC GAGATGCTTG
4101 CCTTTCTCAA TGGGAGGTGG CCTCCCAGGC CTGAAGAAGT CTCCATTTAC
4151 CCCAGAGCCA ACTAGGAAGC AGGTAGACAG CATCATCCCC ACTTATACCC
4201 CAAGGTGCTT GGGGTGAATG GCAGGCCCAA AGCCAAAGCA TGAGACAGAT
4251 TAAATGTTCC TATGGCGAGA GAAGGAGAAG GGTCCACCAG CATCTCTCCA
4301 CTGAGCAAAAT GAAAGGAAGA GAGAAGGCAG GCTGATACCC TCATCAATTT
4351 CCTACTGTCC ATGATATACC ACCATCAACT GGACTTTTTT TTTTTTTTGG
4401 AGATAGAGTC TCGCTTTTGT CACCCAGGCT GGAGTGCAGT GGCATGATCT
4451 CAGTCACTG CAACCTCCAT CTCCCAGGTT CAAGTGATTG TCCCGCTCA
4501 GCCTCCTGAG TAGCTGGGAT TACAGGTGCC TGCTACCACA TCCAGCTGAT
4551 TTTTTTTGTA TTTTATAGTAG AGATGGGGTT TCTTCTTTT TTTTTTTTTT
4601 TTTTGAGACG GAGTCTTGCT CTGTCGCCCA GGCTGGAGTG CAGTGGCGCG
4651 ATCTCGGCTC ACTGCAACCT CCGCCTCCCA GGTTACGCC ATTCTCCTGC
4701 CTCAGCTCC CAGTAGCTG GGACTACAGG CACCTGCCAC CACACTCGGC
4751 TAATTTTTTG TATGTTTAGT AGATATGGGG TTCTACTGCT GTCTCAACCT
4801 TCTGACCTCA TGATCCGCCC GCCTCGGCC CTCAAAGTGC TGGGATTACA
4851 GGCATGAGCG ACTGTGCCG GCCTTTTTTT TTTTTTTTGA GATGGAGTCT
4901 CGCTCTGTCG CCCAGGCTGG AGTGCAATGC CACAATCTCA GCTCACTGCA
4951 AGCTCCACCT CCGAGGTTCA CGCCATTCTC CTGCCTCAGC CTCCTGAGTA
5001 GCTGGGACTA CAGGCGCCCG CCACCACGCC CAGCTAATTT TTTGATTTTT
5051 TAGTAGAGAC GGGGTTTTCAC CTTGTTAGCC AGGATGGTCT TGATCTCCTG
5101 ACCTCGTGAT ACCTCGCTT CAGCCTCCCA AAGTGCTGGG ATTACAGGTG
5151 TGAGCCACCA TGCCTGGCCT TTTTTTTTTT TTTAAGACAG GAGTGTGGTG
5201 GCACAATCTC AGCTCACTGC AACCTCCCC TCTAGGTTCA AGCAATTCTC
5251 CTGCCTCAGC TTTCTAAGTA TAGTAATAGC TGGGACTATA GGCGCCACC
5301 ACCACGCCC GCTAATCTTT TGTATTTTTA GTAGAGATGG GGTTCACCA
5351 TGTTGGCCAG GCTGGTCTCG AATTGCTGAC CTCAAGTGAT CTGCCCACCT
5401 GGGCCTCCCA AAGTGCTGGG ACTATAGGCG GGAGCCACCG CGCCCAGCCT
5451 GGACTCTTTT TAATGAAGCC TTCAAAAAA CTCCTTTTCT CAGCGCTTCT
5501 TACTCTCTGA AACAGACTCT CCACTCTGCT AACCTGCCT CTCACACTGT
5551 GGAACCTAAC CGGATCTTTT TATTCTGAAT CCACAACGTG AAGTACTTGT
5601 CCTCTGTCTA TCGATGGCTA CCTGTGTTTT GAAGTGTTTT TATGGGAATG
5651 AAGCACTGGA GGGGAGGAAA TCAGGCCAGT TCTAGAAGTA GAAGGAAGGC
5701 GAAGAAACCA GGAATAATAT TTATGTGATG GGAGGAAAGG CAGTTTATAA
5751 ATCACTCATG GATCTCTATG CCAGAGGGAT GTGTGAGACA CACGCATGCA
5801 CACACACACT GACTTGCAGG TACATGCAGA GGCAGAAACA AGTCAGGACA
5851 TGACACATAC ATGAATACAC ATACCATCT CATCAGAAAC CAGTCAGAGC
5901 AGAGGGGCCC TGCTTGAGC AAGGAGACTG GAATTTATTC CCCTCTCTCT
5951 CTCAAAGGGT AATTTTGCTG CCTCCATGTC TAGGTTCCCC ACAGATCTGG
6001 CTGCCTCAGA CAGGGGCCCT GGTCTGGTGG CTGGACTCAG CCTGGAGGTC
6051 TTCACAGATG GAGGCCTATA AGAGGTGGCA GCTGACACCT GGAGGGAGCT
6101 GGATGAAAGC AGGCAGTGCA GAGTAGAGAA AGCCAGGTGG TGGGGAGGG
6151 AGTGAGGGAG AAGAGGGGAC CAGATTCAAG CAGCCTTGCG CTGGTTCTAA
6201 AATGGCCACA GCAAGGCAAC GGACAGATGG TCCCTTTCTG ATGCTGAGCC
6251 GGGGAAGTGG GGAAAGGGAA AAGGAAAAA TAAACACCAT CACAGTCAGA
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(SEQ ID NO:3)

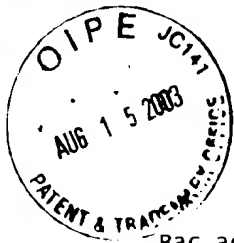
FEATURES:

Start: 3000
Exon: 3000-3614
Stop: 3615

CHROMOSOME MAP POSITION:

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FIGURE 3B



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Bac accession number: AC005973
Chromosome 17

ALLELIC VARIANTS (SNPs):

DNA				
Position	Major	Minor	Domain	
559	-	A T	Beyond	ORF(5')
3638	G	C	Beyond	ORF(3')
5446	C	T A	Beyond	ORF(3')
5808	A	G	Beyond	ORF(3')
5892	A	C	Beyond	ORF(3')
6071	A	G	Beyond	ORF(3')

Context:

DNA
Position

559 CCCTTCCCTCTGTACCCCGCTCCGCATGCGGCAAGTAGTTCGCGACGCGACCCCTTCCCC
CTGTACCCCGCTCCGCATGGGGCCAGTAGTTCGCGACGCGCCCTTCCCTCTGTACCC
GCTCCGCATGCGGCAAGTAGTTCGCGACGCGCCCTTCCCTCTGTACCCGGCTCCGCAT
GCGGAAAGTAGTTCCTACGGTGTGGTTTGCATGTAGATGAAACCCTTTGAGGGGTAAA
GGTTTTTTTTTAAGTACTTTAGCAAATGCAAAGTGTATTATCAATATTAGCCAGCATC
[-,A,T]
TTTTTTTTTTTTTTTTTTTTTTTTTTTTGAGATGGAGTTTCGCTCTTGTCAACCAGGCTGGA
GTGCAATGGCAAAATCTAGGCTCACTGCAACCTCCGCTCCCAAGTTCAGCGATTCTCC
TGCTCAGCCTCCAGGTAGCTGGGATTACAGGCGTGTGCAACCACACCCAGCTAATTTT
TGTATTTTGTAGTAGAGACAGGGTTTACCATGTTGGCCAGGCTGGTCTCGAACTCCTGAC
CTCATGTGATCCATCCGCTCAGCCTCCCAAAGTGTGGGATTACGTAGCCAGTGTCTTT

3638 GTGTGGCACTGCCAGCAGCCCCGACTATTTGTAGGCATGATACTGATCCTCATCTTTGC
CAAGGTGCTCATTCTCTCACAAAGCAGCCCCCTCTCAAAACCCACCAGTCAAGAATACG
ATGTAAAGACCACCCCTCCTCATTCCGGAACAAACAGCCTGACACGCATGTGCTGGGCAG
CTGGCCCTCAGTAGTTGATCTTCTAAGTGTACAGTGTCTCGTGTTCATCGTCTGTTGGC
CAGGCCTTGCCCCCTCCGCCCCATGCTGTGGACATCTGAACCTACTCATCACCATCCA
[G,C]
GTCCCCGACCAGTGAGGACTCAGGCCCTGGATGCCCCACCCATCTCCCTTGAGTACTCT
ATGTATAAGGATGAATTAGAGTTGTCTTTCTCTTCATTAGATATTTATAAAGATTTGG
CCTGTCCATACCCCTGTGGAGCAGCCCTCATCTCCACCTATCTGTACGTATGGAGGT
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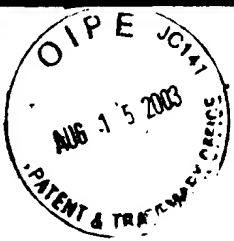
5446 AGGTGTGAGCCACCATGCCTGGCCTTTTTTTTTTTTTTAAGACAGGAGTGTGGTGACA
ATCTCAGCTCACTGCAACCTCCCCTTCTAGGTTCAAGCAATTCTCCTGCCTCAGCTTCT
AAGTATAGTAATAGCTGGGACTATAGGCGCCACCACACGCGCGCTAATCTTTTGTAT
TTTTAGTAGAGATGGGGTTTACCATGTTGGCCAGGCTGGTCTCGAATTGCTGACCTCAA
GTGATCTGCCACCTGGGCTCCCAAAGTGTGGGACTATAGGCGGGAGCCACCGCGCCC
[C,T,A]
GCCTGGACTCTTTTTAATGAAGCCTTCAAAAAAAGTCTTTTCTCAGCGCTTCTTACTCT
CTGAAACAGACTCTCACTCTGCTAACCTGCCTCTCACACTGTGGAACCTCAACCGGATC
TTTTTATTCTGAATCCACAACGTGAAGTACTTGTCTCTGTCTATCGATGGCTACCTGTG
TTTTGAAGTGTTTTTATGGGAATGAAGCACTGGAGGGGAGGAAATCAGGCCAGTTCTAGA
AGTAGAAGGAAGGCGAAGAAACAGGAAAAATATTTATGTGATGGGAGGAAAGGCAGTTT

5808 TGAACAGACTCTCACTCTGCTAACCTGCCTCTCACACTGTGGAACCTCAACCGGATCT
TTTTATTCTGAATCCACAACGTGAAGTACTTGTCTCTGTCTATCGATGGCTACCTGTG
TTTGAAGTGTTTTTATGGGAATGAAGCACTGGAGGGGAGGAAATCAGGCCAGTTCTAGAA
GTAGAAGGAAGGCGAAGAAACAGGAAAAATATTTATGTGATGGGAGGAAAGGCAGTTTA
TAAATCACTCATGGATCTCTATGCCAGAGGGATGTGTGAGACACACGCATGCACACAC
[A,G]
CTGACTTGCAAGTACATGCAGAGGCAGAAACAAGTCAAGGACATGACACATACATGAATAC
ACATACCATTTCTCATGAAACAGTCAAGAGCAGAGGGGCCCTGCCTGGAGCAAGGAGAC
TGGAATTTATTTCCCTCCTCTCAAGGGTAATTTTGTGCTGCCTCCATGTCTAGGTTCC
CCACAGATCTGGCTGCCTCAGACAGGGGCCCTGGTCTGGTGGCTGGAAGTCAAGCCTGGAGG
TCTTCACAGATGGAGGCTATAAGAGGTGGCAGCTGACACCTGGAGGGAGCTGGATGAA

5892 AGTACTTGTCTCTGTCTATCGATGGCTACCTGTGTTTTGAAGTGTTTTTATGGGAATGA
AGCACTGGAGGGGAGGAAATCAGGCCAGTTCTAGAAGTAGAAGGAAGGCGAAGAAACAG

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FIGURE 3C



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Inventors: LI, Zhenya et al.

Title: ISOLATED HUMAN TRANSPORTER...

GAAAAATATTTATGTGATGGGAGGAAAGGCAGTTTATAAATCACTCATGGATCTCTATGC
CAGAGGGATGTGTGAGACACACGCATGCACACACACACTGACTTGCAGGTACATGCAGAG
GCAGAAACAAGTCAGGACATGACACATACATGAATACACATACCATTCTCATCAGAAACC
[A, C]

GTCAGAGCAGAGGGGCCCTGCCTGGAGCAAGGAGACTGGAATTTATTCCCCTCCTCCTCT
CAAAGGGTAATTTTGTGCTGCCTCCATGTCTAGGTTCCCCACAGATCTGGCTGCCTCAGACA
GGGGCCCTGGTCTGGTGGCTGGACTCAGCCTGGAGGTCTTACAGATGGAGGCCTATAAG
AGGTGGCAGCTGACACCTGGAGGGAGCTGGATGAAAGCAGGCAGTGCAGAGTAGAGAAA
CCAGGTGGTGGGGAGGGAGTGAGGGAGAAGAGGGGACCAGATTCAAGCAGCCTTGCGCT

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CCAGAGGGATGTGTGAGACACACGCATGCACACACACACTGACTTGCAGGTACATGCAGA
GGCAGAAACAAGTCAGGACATGACACATACATGAATACACATACCATTCTCATCAGAAAC
CAGTCAGAGCAGAGGGGCCCTGCCTGGAGCAAGGAGACTGGAATTTATTCCCCTCCTCCT
CTCAAAGGGTAATTTTGTGCTGCCTCCATGTCTAGGTTCCCCACAGATCTGGCTGCCTCAGA
CAGGGGCCCTGGTCTGGTGGCTGGACTCAGCCTGGAGGTCTTACAGATGGAGGCCTATA
[A, G]

GAGGTGGCAGCTGACACCTGGAGGGAGCTGGATGAAAGCAGGCAGTGCAGAGTAGAGAAA
GCCAGGTGGTGGGGAGGGAGTGAGGGAGAAGAGGGGACCAGATTCAAGCAGCCTTGCGC
TGGTTCTAAAATGGCCACAGCAAGGCAACGGACAGATGGTCCCTTTCTGATGCTGAGCCG
GGGAAGTGGGGAAAGGAAAAGGAAAAAATAAACACCATCACAGTCAGAAATTTAAAAAT
AAACTGAAAAACCTAAAAAATAAACCGT

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FIGURE 3D